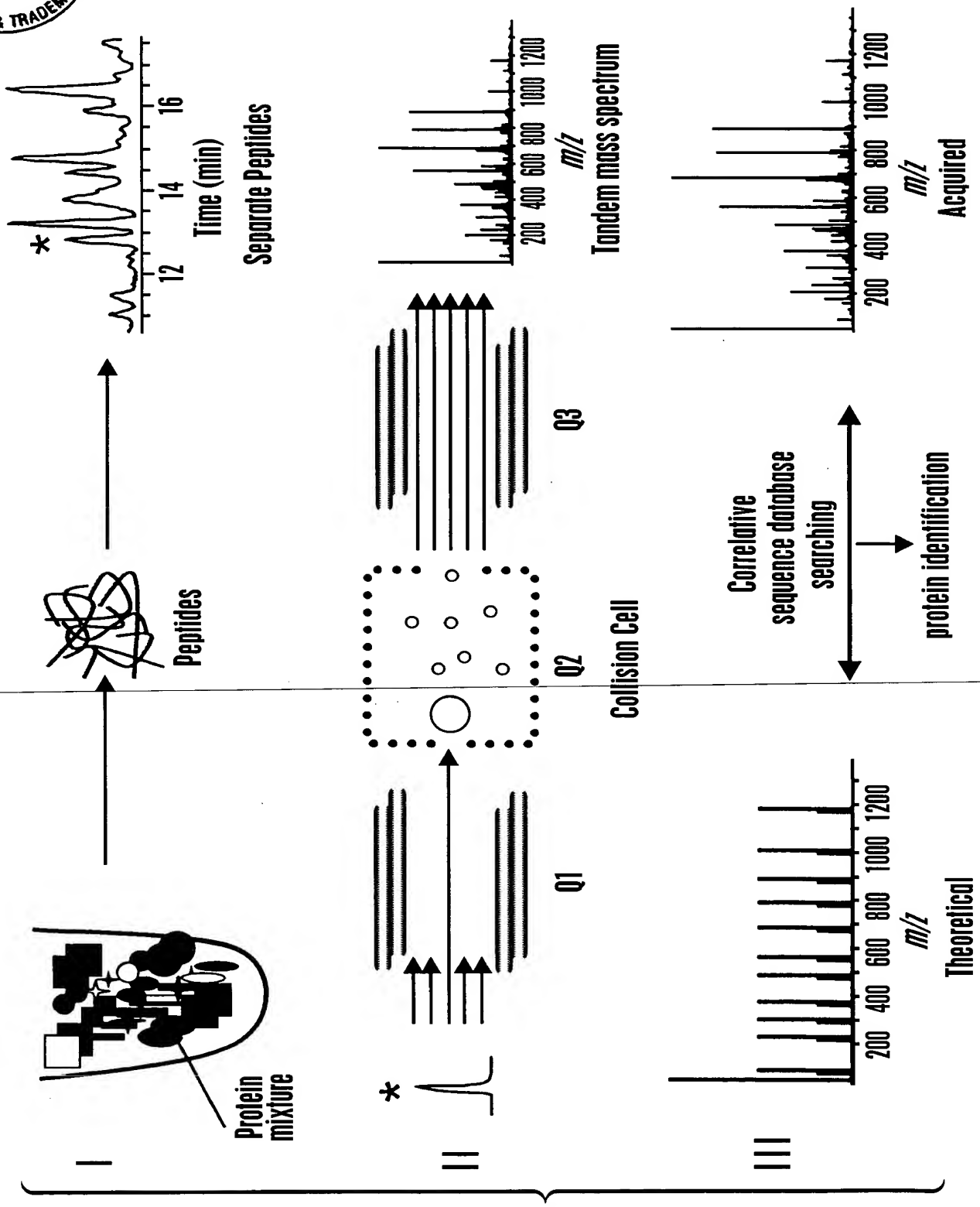

Figure 1

Title: Rapid and Quantitative Proteome Analysis and Related Methods
Inventor: David R. Goodlett
Serial No.: 09/748,783 (Confirmation No. 3333)
Filing Date: December 26, 2000
Attorney Docket: P-IS 4369
USPTO Customer No. 23601 (858-535-9001)

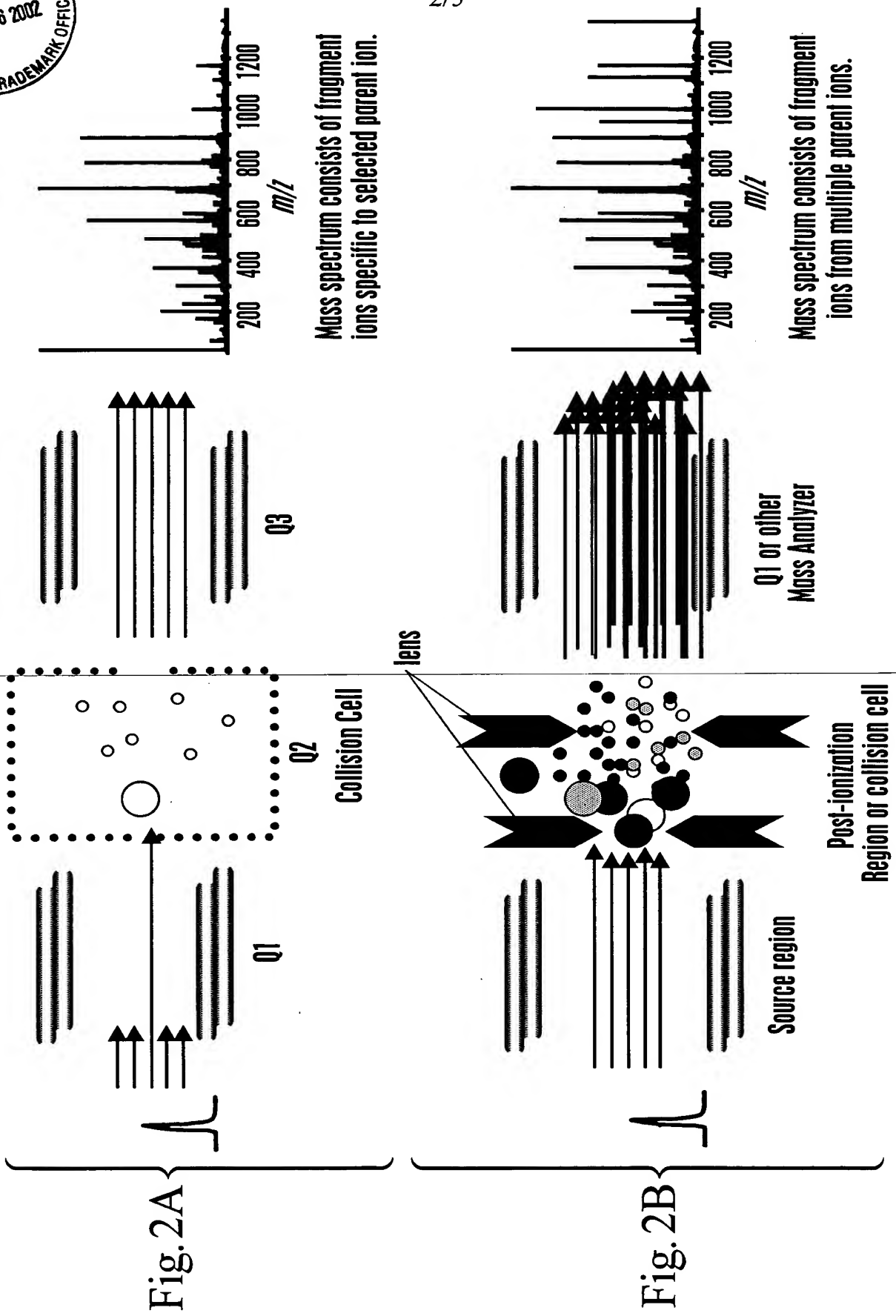

Fig. 2A

Fig. 2B

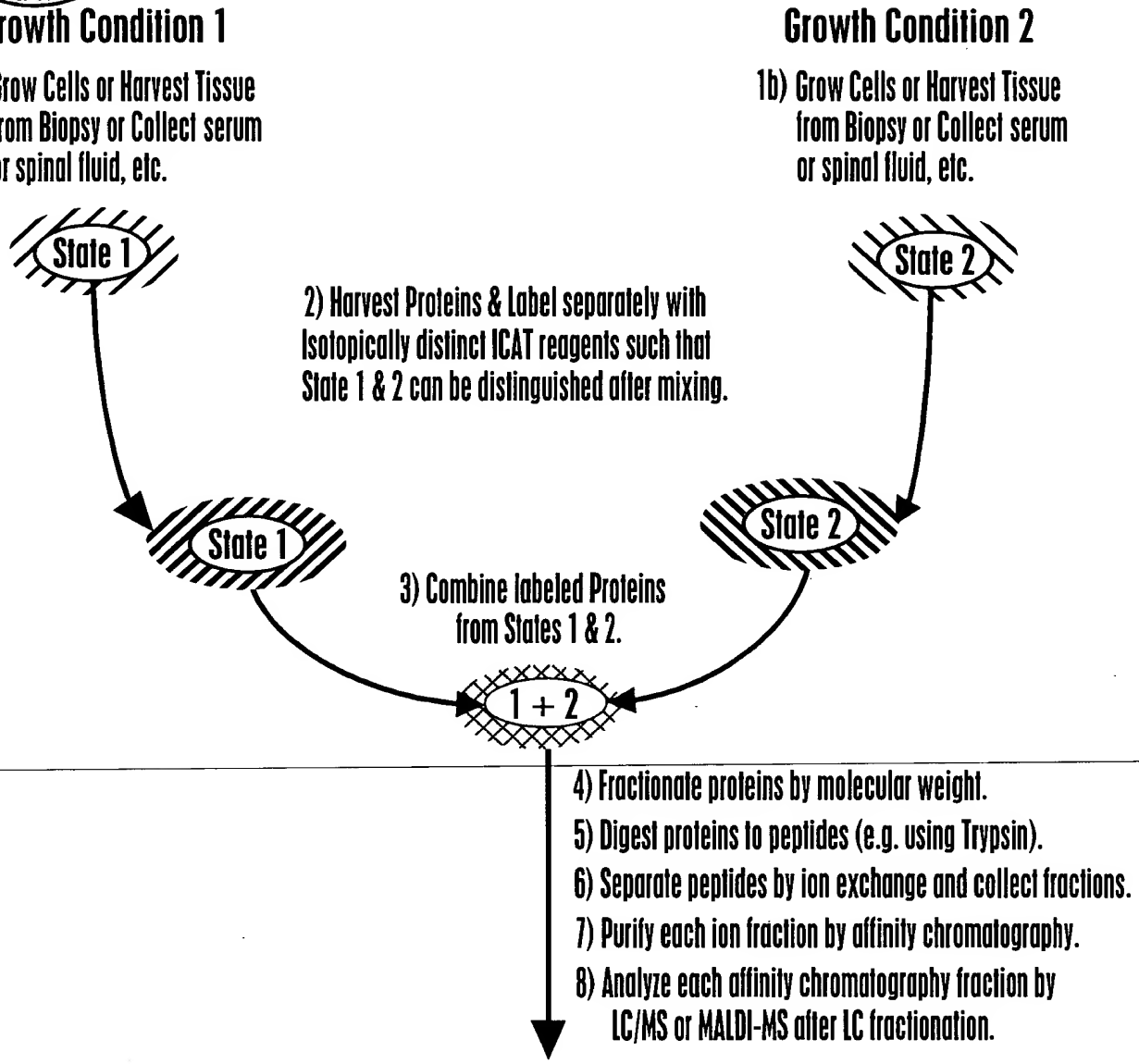

Figure 3

Title: Rapid and Quantitative Proteome Analysis and Related Methods
Inventor: David R. Goodlett
Serial No.: 09/748,783 (Confirmation No. 3333)
Filing Date: December 26, 2000
Attorney Docket: P-IS 4369
USPTO Customer No. 23601 (858-535-9001)

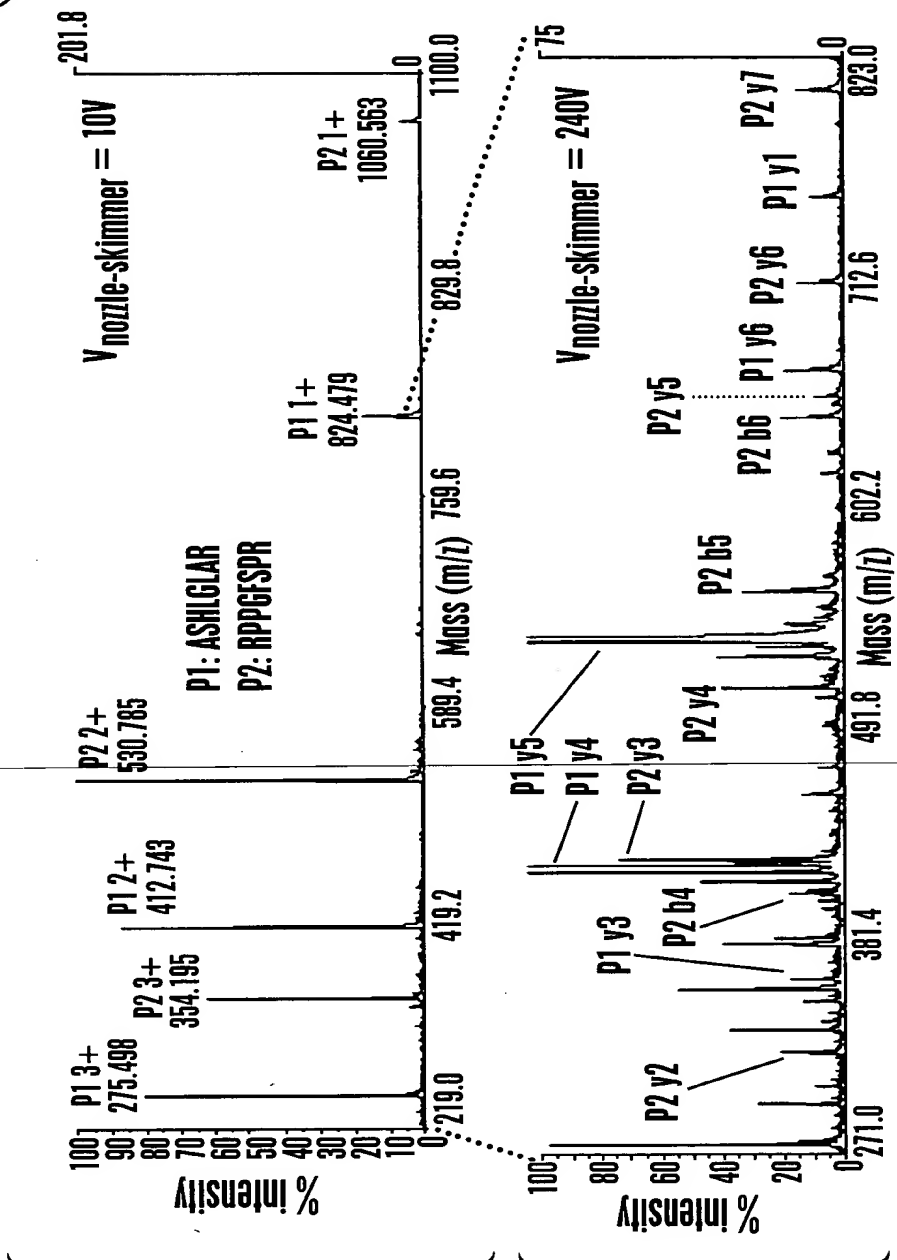

Figure 4A

Figure 4B

Title: Rapid and Quantitative Proteome Analysis and Related Methods
Inventor: David R. Goodlett
Serial No.: 09/748,783 (Confirmation No. 3333)
Filing Date: December 26, 2000
Attorney Docket: P-IS 4369
USPTO Customer No. 23601 (858-535-9001)

Human protein database:
60,884 sequence entries
Fragment ion masses used for analysis:

710.385
753.435
807.374
886.402
904.451
1001.564

Bradykinin RPPGFSPFR MH+ 1060.5676
at 10 PPM, 144 tryptic peptides match
13 matches using fragment ion constraint:

ACISEILPSK
GVRYSFGFK
RANLISQCR
RCGLPSSGKR
RDITLEASR
RERETLEK
RLTEEERK
RLVEVDSSR
RNLLDHHR
RPHAAQPGAR
RPPGFSPFR **
RPQTATASTK
RRPSAYQAL

ASHLGLAR MH+ 824.4739
at 10 PPM, 57 tryptic peptides match
12 matches using fragment ion constraint:

ACYIKVK
ADPLPRR
AFVAFAAK
AFVFGRK
AHAEIRK
AHEAKIR
ALEAHKR
ALQFFAK
AMAIYKK
APDPRLR
ASHLGLAR **
AVAGHLTR

Figure 4C